Bibliographic

Litigation1

Procurement

Fulltext:

Other`

Clerical Prep Time:

Number of Databases:_

Terminal Time:

WWW/Internet

Dialog.

Dr. Link

Westlaw

In-house sequence systems (list)

Other (specify) Computed

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

October 13, 1999, 22:41:30 ; Search time 14.23 Seconds (without alignments) 78.232 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-107-979-4
277
1 HFKPCRDKDLAYCLNDGECF.....SHKHCRCKEGXQGVRCDQFL 47

Scoring table: BLOSUM62

188963 seqs, 23686106 residues Searched:

A_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	use neureaulin	se neurequli	neurequlin	neuregulin		Human neuregulin r	heregulin-1	eregulin-l	Neu differentiatio	ŭ	hereguli	EGFL2. Glial growt	EGFL5. Glial growt	EGFL6. Glial growt	EGFL2. Glial mitog	EGFL5. Glial mitog	EGFL6. Glial mitog	PP2. Glia	GGF2BPP2. Glial gr	GGF2BPP2. Glial mi	GGF2BPP2. Glial mi	Human NDF-alpha3 c	Human NDF-alpha2b	. Human proNDF-alpha	Bovine glial cell	Human epidermal li				Epidermal growth f		Epidermal growth f	BPP2 glial growth	growth	mal	dermal	dermal	-alpha f	differentia	ine neur	. Use of n	. Use	se of ne
SUMMARIES		W9761	762	761	W97621	762	761	545	545	218	53	957	591	592	592	565	266	999	689	591	565	268	856	356	926	724	725	725	725	721	746	746	746	745	376	0	508	507	999	518	W09360	936	936	936
	ngth DB	713	7	20	360 1	47	9	21	20	52	m	50	m	ω,	m	m	ω.	83	m	80	80	63	25	62	~	80	m	æ	83	m	m	œ	83	0	80	m	m	88	S	22	m	m	۵	m
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Human neuregulin G	Rat NRSF. New reco
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280	422
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ALIGNMENTS

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New 199-120882/10.

New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome infection, provides human and murine polypeptides (see also wg7617), a novel member of the ceptor, but not to the ErbB3 receptor, but not to the ErbB3 receptor, but not to the ErbB3 or ErbB3 receptor, but not to the ErbB2 or ErbB3 receptor, but not provides human and murine polypeptides (see also wg7618) that have provides human and murine polypeptides (see also wg7618) that have provides human and murine polypeptides (see also wg7618) that have cells and methods for the recombinant production of novel nost rels and methods for the recombinant production of cells at least 75% homology to the NRG3 ECD, as well as expression vectors, containing the ErbB4 receptor in vivo and in vitro. They can be used to reat damage to a nerve or damage to other NRG3-expressing prevent or treat damage to a nerve or damage to other NRG3-expressing particular, they can be used to treat patients whose containing the ErbB4 receptor in vivo and in vitro. They can be used to reat patients whose nervous system has been damaged by eg. trauma, surgery, stroke, is multiple sclerosis). They can be used to treat patients whose increal armany infection, metabolic disease, nutritional deficiency, conditions involving spinal method of sease. Davin's syndrome, as sortiated with systemic disease. They can also be used to treat of muscular arrophy or paralysis, neurodepane, nerve damage or cell experies. Huntington's chorea, bown's syndrome, nerve damages or disease, abetaling Charles syndrome, nerve damages or the erbling charles with systemic disease including post-polic syndrome, associated with systemic disease. Davin served to treat disease, abetalipo
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                                                                                                                                                                                                                                                                                           Gaps
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Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's disease, metachromatic leukodystrophy, Fabry's disease and Dejerine-Sottas syndrome, to treat disease of skeletal muscle of smooth muscle, such as muscular dystrophy or diseases caused by skeletal or smooth muscle wasting. The products can also be used for detection, diagnosis, for the production of transgenic or knockout animals or for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse neuregulin related ligand NRG3 extracellular domain.
Neuregulin related ligand; NRG3; mouse; ErbB4 receptor;
signal transduction; nervous system disorder; neurodegeneration;
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                                                                                                                                                                                                                                        Length 713;
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                                                                                                                                                                                                                                                                                             Mismatches
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WPI; 99-120882/10.
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24-JUL-1997; US-899437.
09-JUL-1997; US-052019.
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Matches 47; Conserv
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WO9902681-A1.
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                                                                                                                                                                                Sequence
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W97620
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Dr. N-FSDB; XUDBUS.

PT New isolated neurogulin related ligand-3 - used to develop products prove infection, malignancy, Alzheimer's disease or Down's syndrome and infection, malignancy, Alzheimer's disease or Down's syndrome proved infection, malignancy, Alzheimer's disease or Down's syndrome proved infection, malignancy, Alzheimer's disease or Down's syndrome proved in the amino acid sequence of human neuregulin related ligand this is the amino acid sequence of human neuregulin related ligand control of protein ligands that binds to the ErbB receptor, but not control of protein ligands that binds to the brab receptor, but not tyrosine phosphorylation. The sequence was deduced from the nucleotide sequence of a CDNA clone (see X66988) from a foetal brain nucleotide sequence of a CDNA clone (see X66988) from a foetal brain control of NRG3 is provided in W97619. The invention provides of other neuregulins. An alternatively spliced control of the NRG3 polypeptides (see also W9761), expression of control of NRG3 polypeptides (see also W9761), expression of control of the SDB4 receptor in vivo and in vitro. They can be used to nerve the survival, proliferation or differentiation of calls or nevent to treat damage to a nerve or damage to other NRG3-expressing or NRG3-responsive cells.

CC or NRG3-responsive cells, e.g. brain, heart, or kidney cells. In particular, they can be used to treat diseases which involve neural parvicular, they can be used to treat diseases which involve neural cell growth such as demyelination, or damage to treat patients whose nervous system has been damaged by e.g. trauma, surgery, stroke, servement, infection, metabolic disease, nutritional deficiency, created malignancy, or toxic agents. NRG3 can also be used to treat patients.
                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sites for O-linked glycosylation"
                                                                                                                                                                                                                                                                                                                                                                      Human neuregulin related ligand NRG3.
Neuregulin related ligand, NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis.
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      or
                                                                                                      Length 362;
for detection, diagnosis, for the production of transgenic knockout animals or for drug screening. Sequence 362 AA:
                                                                                                                                           0; Indels
                                                                                                                                                                                                  288 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 334
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                                                                                                                                                                                1 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL
                                                                                                    Score 277; DB 1;
Pred. No. 1.9e-21;
; Mismatches 0;
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/note= "EGF-like domain"
356. .394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in Claim 5(a)"
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1. .360
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                                                                                                      100.0%; Sc
100.0%; Pr
tive 0;
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Godowski PJ, Mark MR, Zhang D;
WPI: 99-120882/10.
N-PSDB; X06988.
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                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 47; Conservative
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30-JUN-1998; U13411.
24-JUL-1997; US-899437.
09-JUL-1997; US-052019.
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W97618
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motor neuron disorders such as amyotrophic lateral sclerosis (Lou cerrigo's disease), Bell's palsy, conditions involving spinal muscular atrophy or paralysis, conditions involving spinal cartrophy or paralysis, neurodegenerative disorders such as a lateral series, parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, and Meniere's disease. They can also be used to treat neuropathies cassociated with systemic disease including post-polio syndrome, cassociated with systemic disease including post-polio syndrome, con hereditary neuropathies including Charcot Marie-Tooth disease, Refsum's disease, abetalipoproteinemia, Tangier disease, Consecutation as muscular distractions of skeletal muscle of smooth muscle, such as muscular distractory or diseases caused by consecutation diagnosis, for the products can also be used for detection, diagnosis, for the production of transgenic or smooth muscle wasting. The products can also be used for detection, diagnosis, for the production of transgenic or Sequence 720 AA;
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Gaps ; 0 100.0%; Score 277; DB 1; Length 720; 100.0%; Pred. No. 3.6e-21; Indels 286 HFKPCRDKDLAYCLNDGECEVIETLTGSHKHCRCKEGYQGVRCDQFL 332 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47 Mismatches ó Conservative Similarity 47; Query Match Best Local Н Matches g õ

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New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, an fection, malignancy. Alzheimer's disease or Down's syndrome Claim 30; Page 64: 101pp; English.

This is the epidormal growth factor (EGF)-like domain of human currently referred ligand NRG3 (see also W9761B), a novel member of the EGF-like family of protein ligands that binds to the ErbB4 receptor and activates ErbB4 receptor tyrosine phosphorylation.

The EGF-like family of protein ligands that binds to the ErbB4 receptor and activates ErbB4 receptor tyrosine phosphorylation.

The EGF-like family of NRG3 is distinct from the EGF-like domains of NRG1 and NRE2. The invention provides human and murine polypeptides (see also W97617) that have at least 75% homology to the NRG3 EGF-like domain, as well as expression vectors, nost cells and methods for the recombinant production of novel NRG3. The NRG3 polypeptides and polynucleotides and can be used to enhance the survival, priléferation or differentiation of cells having the ErbB4 receptor in vivo and in vitro. They can be used to prevent or treat damage to a nerve or damage to other NRG3 expression or particular, they can be used to treat patients whose nervous system has be used to treat patients whose nervous system has been damaged by e.g. trauma, surgery, stroke, ischaemia, inferthour metabolic disease, nutritional deficiency, metabolic d Gaps and Meniere's disease. They can also be used to treat neuropathies associated with systemic disease including post-polio syndrome, hereditary neuropathies including Charcot-Marie-Tooth disease, Refsum's disease, abetallpoproteinemia, Tangier disease, Krabbe's disease, metachromatic leukodystrophy, rabby's disease and Dejerine-Sottas syndrome, to treat disease of skeletal muscle smooth muscle, such as muscular dystrophy or diseases caused by skeletal ramooth muscle wasting. The products can also be used for detection, diagnosis, for the production of transgenic or knockout animals or for drug screening. motor neuron disorders such as amyotrophic lateral sclerosis (Lou defaring's disease), Bell's palsy, conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, and Menlere's disease. They can also be used to treat neuropathies associated with systemic disease including post-polio syndrome, hereditary neuropathies including Charcot-Marie-Tooth disease, 10-MAY-1999 (first entry)
Human neuregulin related ligand NRG3 EGF-like domain.
Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin. ö 100.0%; Score 277; DB 1; Length 360; 100.0%; Pred. No. 1.9e-21; 0; Indels 286 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 332 1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47 0; Mismatches 21-JAN-1999. 30-JUN-1998; U13411. 24-JUL-1997; US-899437. 09-JUL-1997; US-052019. GCETH) GENEWYECH INC. GGOWEK! PJ. MARK MR, Zhang D; WPI; 99-120882/10. W97622 standard; Protein; 47 AA 47; Conservative Query Match Best Local Similarity 360 AA; Homo sapiens. WO9902681-A1. Sequence W97622; Matches RESULT W97622 g 88888888888888 ò

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Tor treating nervous system disorders, e.g. stroke, ischaemia,
Tinfection, malighanacy, Alzheimer's disease or Down's syndrome
Example 1: Page 78-81: 101pp; English.
C This is the amino acid sequence of splice variant hNGR3B2 of human
C neuregulin related ligand NRG3, a novel member of the splidermal
growth factor (EGF)-like family of protein ligands that binds to
the ErbB4 receptor, but not to the ErbB2 or ErbB3 receptor, and
which activates ErbB4 receptor tyrosine phosphorylation. The
sequence was deduced from the nucleocide sequence of a cDNA clone
(see X06989) from a foetal brain library. hNGR3B2 lacks amino
acids 529-552 of hNGR3B1 (see W97618) but retains the EGF- like
comain and is expected to exhibit biological activity. The invention
provides human and murine NRG3 polypeptides (see W97617), expression
vectors, host cells and methods for the recombinant production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WRG3s. The NRG3 polypeptides and polynocleotides and can be used to enhance the survival, proliferation or differentiation of cells having the Enb84 receptor in vivo and in vitro. They can be used to prevent or treat damage to a nerve or damage to other NRG3-expressing or NRG3-responsive cells.
                                                                                                                                                                                                                                                                              Gaps
            disease, metachromatic leukddystrophy, Fabry's disease and Dejerine-Sottas syndrome, to treat disease of skeletal muscle of smooth muscle, such as muscular dystrophy or diseases caused by skeletal or smooth muscle wasting. The products can also be used for detection, diagnosis, for the production of transgenic or knockout animals or for drug screening. A claimed immunoadhesin comprises the human NRG3 EGF-like domain fused to an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "extracellular domain, specifically claimed
in Claim 5(a)"
disease, abetalipoproteinemia, Tangier disease, Krabbe's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-1999 (first entry)
Human neuregulin related ligand NRG3 (splice variant).
Neuregulin related ligand, NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; splice variant.
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/note= "EGF-like domain"
356. 394
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1. .360
                                                                                                                                                                                                                                                                                                                                                                                                                                                              W97619 standard; Protein; 696 AA.
W97619;
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Best Local Similarity 100.0
Matches 47; Conservative
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09-JUL-1997; US-052019.
(GETH ) GENENTECH INC.
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Claim 17; Page 86-87; 118pp; English.
This sequence is the human heregulin-like factor (HLF) of the linvention. The HLF is involved in the regulation of cell growth. Detection of disferent levels of expression of the HLF gene can be used for the diagnosis of disorders, e.g. in the neural system. In particular, detection of different levels of HLF gene expression in cell or body fluid of an individual can be used for diagnosing cancer. The products can also be used in the treatment of disorders involving abnormal levels of HLF activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-1999 (first entry)
Human heregulin-like factor sequence.
Human heregulin-like factor; HLF; cell growth regulator; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated heregulin-like factor - used to develop products for the diagnosis and treatment of disorders involving regulation of cell growth, particularly cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Y05451 standard; Protein; 157 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neural system disorder; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIV GEORGETOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-1998; U12403.
17-JUN-1997; US-049942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 99-09521,
N-PSDB; X36423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
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Length 52;

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Query Match
Best Local Similarity 33.38
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterfield MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9218627-A.
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                                                                                                                                                                                                                                                                                                                                           18-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-1992
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                                                                                                                                                        g
                                                                                                                                                                                                                                                                                             δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                        the diagnosis and treatment of disorders involving regulation of cell growth, particularly cancers

PT the diagnosis and treatment of disorders involving regulation of cell growth, particularly cancers

PS bisclosure; Page 97-99; 118pp; English.

CC This sequence is the human heregulin-like factor (HLF) of the CC invention. The HLF is involved in the regulation of cell growth.

CC invention of different levels of expression of the HLF gene can be used for the diagnosis of disorders, e.g. in the neural system. In CC particular, detection of different levels of HLF gene expression in cells or body fluid of an individual can be used for diagnosing cancer. The products can also be used in the treatment of disorders involving sequence 720 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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The peptides W05182-W05185 are based on neu differentiation factor (NDF)/heregulin alpha and beta form EGF-like domains in various combinations. The peptides maintain the survival and proliferation of Schwann cells and cause proliferation, growth and differentiation of colon epithelial cells. Accordingly, they are useful to treat (in vitro or in vivo) a disease or disorder of the colon (e.g. colitis or an ulcer) or of the nervous system (e.g. nerve damage caused by trauma). Sequence 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1997 (first entry)
Neu differentiation factor/heregulin-alpha/beta form EGF-like domain.
NDF: neu differentiation factor; heregulin; epidermal growth factor;
EGF; colon epithelial cell proliferation; Schwann cell; nerve;
damage; colitis; ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                  Human heregulin-like factor sequence.
Human heregulin-like factor; HLF; cell growth regulator; diagnosis; neural system disorder; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 277; DB 1; Length 720; 100.0%; Pred. No. 3.6e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cranahan JF, Hara S, Lu HS, Mayer JP, Yoshinaga SK;
WPI; 96-465022/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Hijazi MM, King CR, Ruben SM, Young P;
WPI; 99-095327/08.
New isolated heregulin-like factor - us
                                                                            standard; Protein; 720 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08; FAY
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                                                                                                                                                                                                                                                                                                             16-JUN-1998; U12403.
17-JUN-1997; US-049942.
(HUMA-) HUMAN GENOME SCI INC.
(GEOU ) UNIV GEORGETOWN.
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 47; Conservative
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27-MAR-1996; U04262.
06-APR-1995; US-417640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
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                        RESULT
                                                                                                    AND DESCRIPTION OF THE PROPERTY OF THE PROPERT
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Disclosure; Fig 28b; 98pp; English.

The sequences given in R28536-38 are encoded by CDNA sequences which have been derived from the putative bowine glial growth factor-II (GGF-II) CDNA by alternative splicing. The bovine GGF-II cDNA sequence was isolated by probing a bovine cDNA library with the sequence given in G30583-616 which were designed by backtranslating amino acid sequences derived from purified GGF-II protein. Isolated open reading frames were amplified using polymerase chain reaction on pituitary RNA Gsee also Q30683-667). The isolated sequence was found to contain at least five exons and three alternative splice patterns could be used to produce the putative bovine GGF-II CDNA sequences 1,
                                                                                                                                                                                                                                                                                                                                                                      GGF2BPP2.CDS protein.
Glial growth factor-II; GGF-II; backtranslation; bovine cDNA library;
polymerase chain reaction; PCR; amplify; pituitary RNA; exons;
alternative splice pattern.
                                                      Gaps
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p185-HER2 ligand: her2 proto-oncogene; breast cancer; EGF receptor;
epidermal growth factor; tyrosine kinase-like glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glial mitogenic polypeptide factors - used in diagnosis, prophylaxis or treatment of patho-physiological conditions of the
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nes 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 HLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-0CT-1992.
03-APR-1992; G00595.
10-APR-1991; GB-007566.
(CAMB-) CAMBRIDGE NEUROSCIENCE INC.
(LUDW-) LUDWIG INST CANCER RES.
Goodearl ADJ, Marchionni MA, Minghetti L, Stroobant P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                      1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQFL
42.1%; Score 116.5; DB 1; 33.3%; Pred. No. 8.2e-06; iive 15; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.0%; Score 113.5;
34.8%; Pred. No. $7.46
tive 14; Mismatches
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/label= transmembrane
/note= "probable"
226. .265
/label= EGF_motif
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R29570;
                                                                                                                                                                                                                                                                                         R28537 standard; Protein; 263 AA
                                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity
Matches 16; Conserv
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N-PSDB; Q30670.
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erbB2 receptor;

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Glial growth factor DNA encoding numerous polypeptide factors used for inhibiting cell proliferation - for treating carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                    and nervous disorders.

Disclosure; Fig. 40; 178pp; English.
The GGF coding segments include regions with EGF-like homology.
These EGF-like domains can be required for the activation of mitogenesis in the binding reaction between GGF ligands contg. such domains and the erbB2 receptor. Pref. antiproliferative factors are those which lack these EGF-like domains.
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                      Glial growth factor; GGF; heregulin; mitogenesis; Schwann cell; tumour; central nervous system; erbantiproliferative; epidermal growth factor; EGF. WO9403644-A.
                                                                                                                                                                                                                                                                                     (CAMB-) CAMBRIDGE NEUROSCIENCE INC.
GWynne DI, Marchionni M, McBurney RN;
WPI: 94-065731/08
N-PSDB; 058324.
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                                                                                                                                                                                 US-927337.
US-951747.
                                                                                                                                                                                                       25-SEP-1992; US-951747.
01-DEC-1992; US-984085.
29-JAN-1993; US-011396.
                                                                                                                                                        U07491
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Matches 16; Conserv
                                                                                                                                                        10-AUG-1993;
10-AUG-1992;
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R46921
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T antagonists for binding to P185HBR2

Example 3: Fig 4: 139pp; English.

C carcinoma MDA-MB-231. After purification, a major peak of tyrosine phosphorylation activity was correlated with a 45kD protein. The protein was cleaved with Lysine-C and one of the resulting peptide fragments (C-15) was used to design an oligonucleotide probe (see C q31547). The probe was labelled and used to screen an oligon of Trimed cDNA library constructed from human MDA-MB-231 cell mRNA in lambda g110. Two positive clones, designated lambda g110 her13, were identified and found to be identical. The sequence of lambda g10 her16 contains a single ORF of 669 amino acids. No stop door was found in the translated sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "deduced from ORF but initiating MET
                                                                                                                                                                                                          151. 152
/note= "serine-glycine dipeptide potential
glycosaminoglycan addition site"
                                                                                                                                        /note= "serine-glycine dipeptide potential glycosaminoglycan addition site" 151. .152
                                                 /note= "serine-glycine dipeptide potential glycosaminoglycan addition site -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 437. .439
/note= "N-linked glycosylation site"
609. .611
/note= "N-linked glycosylation site"
209. .221
/note= "serine-threonine potential
0-glycosylation sites"
                                                                                                   not part of mature HRG-alpha sequence"
                                                                                                                                                                                                                                                                                                                                                                   note="N-linked glycosylation site"
108. 210
note="N-linked glycosylation site"
                                                                                                                                                                                                                                                                                  164...166
/note= "N-linked glycosylation site"
170...172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at position 45 and the processed N-terminal residue is Ser46"
"contains 6 cysteines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 34.89
Matches 16; Conservative
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24-MAY-1991; US-705256.
25-SEP-1991; US-705212.
08-NOV-1991; US-765212.
06-MAR-1992; US-847743.
11-MAY-1992; US-880917.
(GENE-) GENETECH INC.
Holmes WE, Vandlen RL;
                      .43
/note=
42. .43
/note=
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Gaps

1;

41.0%; Score 113.5; DB 1; Length 63; 34.8%; Pred. No. 2e-05;

Mismatches

14;

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                                                                                                                                                                                                                                                                                                                          Glial growth factor DNA encoding numerous polypeptide factors used for inhibiting cell proliferation - for treating carcinoma
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 43; 178pp; English.

The GGF coding segments include regions with EGF-like homology. These EGF-like domains can be required for the activation of mitogenesis in the binding reaction between GGF ligands contg. such domains and the erbB2 receptor. Pref. antiproliferative factors are those which lack these EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                               Glial growth factor; GGF; heregulin; mitogenesis; Schwann cell; tumour; central nervous system; erbB2 receptor; antiproliferative; epidermal growth factor; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.0%; Score 113.5; DB 1; Length 88; 34.8%; Pred. No. 2.7e-05; tive 14; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                    (CAMB-) CAMBRIDGE NEUROSCIENCE INC.
Gwynne DI, Marchionni M, McBurney RN;
R46921 standard; Protein; 88 AA.
                                 28-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                           10-AUG-1992; US-927337.
25-SEP-1992; US-951747.
01-DEC-1992; US-984085.
29-JAN-1993; US-011396.
                                                                                                                                                                                                                                                                                                                                                               and nervous disorders
                                                                                                                                                            10-AUG-1993; U07491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 16; Conserv
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N-PSDB; Q58327.
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R46918 standard; Protein; 63 AA. R46918; 28-JUL-1994 (first entry)

RESULT 12 R46918

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                                                                                                                                                                                                                                                                                                                                 Glial growth factor DNA encoding numerous polypeptide factors used for inhibiting cell proliferation - for treating carcinoma and nervous disorders
Disclosure; Fig 44, 178pp; English.

The GGF coding segments include regions with EGF-like homology.
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                                                                                                                                                                                                                                                                                                                                                                                                       These EGF-like domains can be required for the activation of mitogenesis in the binding reaction between GGF liquids confq. such domains and the erbb2 receptor. Pref. antiproliferative factors are those which lack these EGF-like domains.
                                                                                                                                                     Schwann cell; tumour; central nervous system; erbB2 receptor; antiproliferative; epidermal growth factor; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glial mitogenic polypeptide factors - useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glial growth factor; GGF; heregulin; mitogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 41.0%; Score 113.5; DB 1; Best Local Similarity 34.8%; Pred. No. 2.6e-05; Matches 16; Conservative 14; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glial growth factor; GGF; heregulin; mitogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schwann cell; tumour; central nervous system; epidermal growth factor; EGF. WO9400140-A.
                                                                                                                                                                                                                                                                            (CAMB-) CAMBRIDGE NEUROSCIENCE INC.
Gwynne DI, Marchionni M, McBurney RN;
WPI: 94-065731/08
N-PSDB; 058328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R55659 standard; Protein; 63 AA.
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                                                                                 R46922 standard; Protein; 83 AA.
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P, Waterfield M;
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28-JUL-1994 (first entry)
                                                                                                           28-JUL-1994 (first entry)
EGFL6.
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US-927337.
US-951747.
US-984085.
US-011396.
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03-SEP-1992; US-940389.
23-OCT-1992; US-965173.
24-MAR-1993; US-036555.
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N-PSDB; Q62843.
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29-JAN-1993;
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R55659
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63 AA;
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41.0%; Score 113.5; DB 1; 34.8%; Pred. No. 2e-05; tive 14; Mismatches 15;
       vuery match . 41.09
Best Local Similarity 34.89
Matches 16; Conservative
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Search completed: October 13, 1999, 22:45:05 Job time: 215 sec

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              Compugen Ltd
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Copyright (c) 1993 - 1998 Comp
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MEDLINE; 97420720.

ZEHANG D. (SELUKKOKI M.X. (SMARK M., FRANTZ G., AKITA R., SUN Y., CHILLAN K./SCROWLEY C. (ZERUSH J./(SCDOWSKI P.J.;

CHILLAN K./SCROWLEY C. (ZERUSH J./(SCDOWSKI P.J.;

Neurequin-3 (NRG3): a novel neural tissue-enriched protein that binds and activatus ErbB4.";

Proc. Natl. Acad. Sci. U.S.A. 94:9562-9567(1997).

FEMBL; AR010130; AABD914.1; -.

MGD; MGI:1097165; NRG3.
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Eukaryota; Metagou; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Arta Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
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                         Q92015
P70628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 98352126.
YANG J.F., ZHOU B., PUN S., IP N.Y., PENG H.B., TSIM K.W.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 334
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                    092015
P70628
035727
015122
015816
014902
P78504
090819
063722
061521
020559
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014944
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Glycoprotein.
SEQUENCE 71
Xenopus.
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093383
1D 093
AC 099
DT 011
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PRELIMINARY;
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PDB; 1HRF; 15-OCT-94
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Q02297;
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"Cloning of cDNAs encoding xenopus neuregulin: expression in myotomal muscle during embryo development.";
Brain Res. Mol. Brain Res. 58:59-73(1998).
PRAM: AF076618; AAC26804.1;
PFAM; PF00008; EGF: 1.
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WEND D., SUGGS S.V., KARUNAGARAN D., LIU N., CUPPLES R.L., LUO Y., JANSEN A.M., BEN-BARUCH N., TROLLINGER D.B., JACOBSEN V.L., MENG S.Y., LU H.S., HU S., CHANG D., YANGAHARA D., KOSKI R.A., YARDEN Y.;

SITURCULARIAL AND functional aspects of the multiplicity of Neu differentiation factors.";

MOI. Cell. Biol. 14:1909-1919(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE: 94158663.
WED D., SUGGS S.V., KARUNAGARAN D., LIU N., CUPPLES R.L., LUO Y.,
WEN D., SUGGS S.V., BEN-BARCH N., TROLLINGER D.B., JACOBSEN V.L.,
MENG S.Y., LU H.S., HU S., CHANG D., YANG W., YANIGAHARA D.,
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                                                                                                                                                                                                                     Length 677;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 462;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
NEU DIFFERENTIATION FACTOR (FRAGMENT).
                                                                                                                                                                                                                DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match · 41.0%; Score 113.5; DB 4; Best Local Similarity 34.8%; Pred. No. 1.5e-07; Matches 16; Conservative 14; Mismatches 15;
                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                Query Match

45.7%; Score 126.5; DB 1
Best Local Similarity 43.5%; Pred. No. 3.9e-09;
Matches 20; Conservative 10; Mismatches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
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SEQUENCE 46
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SEQUENCE 67
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Q12780;
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Q12780
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Q12781
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                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A, AND SEQUENCE OF 2-22 AND 182-205.

BDLINE, SZINKOWSKI M.X., AKITA R.W., HENZEL W.J., LEE J.,
HOLMES W.E., SLIWKOWSI M.X., ARAIA R.W., HENZEL W.J., LEE J.,
PARK J.W., YANSURA D., ABADI N., RAAB H., LEWIS G.D., SHEPARD H.M.,
RANGN G.W., WOOD W.I., GOEDDEL D.V., VANDLEN R.L.,
"Identification of heregulin, a specific activator of pl85erb82.";
Science 256:1205-1210(1992).
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KOSKI R.A., YARDEN Y.,
"Structural and functional aspects of the multiplicity of Neu
differentiation factors.";
MAI. Cell. Biol. 14.1909-1919(1994).
EMBL; U021277, AAB19522.1;
PFAM; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                            Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 640;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 175-241.
NAGATA K., KOHDA D., HATANAKA H., ICHIKAWA S., MATSUDA : YAMAMOTO T., SUZUKI A., INAGARI F.;
SUDMILTEC (JUL-1994) to the PDB data bank.
-! SIMILARITY: BELONGS TO EGF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                   56 HLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HERECULIN-ALPHA (HRG-ALPHA).
                                                                                                                                                                                                                                                                                            Query Match 41.0%; Score 113.5; DB 4; Best Local Similarity 34.8%; Pred. No. 4.2e-08; Matches 16; Conservative 14; Mismatches 15;
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                                                                                                                                                            70391 MW; 7A13DF1C CRC32;
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EGF-like domain
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PFAM; PF00008; EGF; 1.
PFAM; PF00047; 19; 1.
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MEDLINE; 92257596.
WEN D., PELES E., CUPPLES R., SUGGS S.V., BACUS S.S., LUO Y.,
TRAIL G., HU S.; SILBIGER S.M., LEVY R.B.;
"Neu differentiation factor: a transmembrane glycoprotein containing
an EGF domain and an immunoglobulin homology unit.";
Cell 69:559-572(1992).
-!- SMILARIY: 3ELONGS TO EGF FAMILY.
                                                                                                                                                                                           "SEQUENCE FROM N.A.

"SEQUENCE FROM N.A.

"SEQUENCE FROM N.A.

"MEDLINE; 94158863.

"A WEND., SUGGS S.V., KARUNAGARAN D., LIU N., CUPPLES R.L., LUO Y.,

"A WEND., SUGGS S.V., HU S., HU S., CHANG D., XANG W., YANIGAHARA D.,

"A KOSKI R.A., YARDEN Y.;

"A KOSKI R.A., YARDEN Y.;

"Gructural and functional aspects of the multiplicity of Neu
"Tructural and functional aspects of the multiplicity of Neu
"Tructural and L1:1909-1919(1994).

"I "Gructural ELONGS TO EGF FAMILY.

"EMBL, U02316; AAA19941.1; ".

"EMBL, U02316; AAA19942.1; ".

"EMBL, U02316; AAA19942.1; ".

"EMBL, U02316; AAA19942.1; ".

"EMBL, U02316; AAA19942.1; ".

"EMBL, U00316; EGF; 1.

"EMBL, U00016; EGF; 1.

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MEDLINE; 9415863.
MEDLINE; 9415863.
MEN D., SUGGS S.V., KARUNAGARAN D., LIU N., CUPPLES R.L., LUO Y., JANSEN A.M., BEN-BARUCH N., TROLLINGER D.B., JACOBSEN V.L., MENG S.Y., LU H.S., HU S., CHANG D., YANG W., YANIGAHARA D., KOSKI R.A., YARDEN Y.;
"Structural and functional aspects of the multiplicity of Neu differentiation factors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 461;
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 HLIKCAEKEKTFCVNGGECFTVKDLSNPSRYLCKCQPGFTGARCTE 223
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
NEU DIFFERENTIATION FACTOR NDF19.
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Last annotation update)
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40.3%; Score 111.5; DB 11;
Best Local Similarity 34.8%; Pred. No. 2.7e-07;
Matches 16; Conservative 13; Mismatches 16;
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EMBL; M92430; -; NOT_ANNOTATED_CDS.
PROSITE; PS00022; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEU DIFFERENTIATION FACTOR NDF44.
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PFAM; PF00047; iç; 1.
Transmembrane; EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08,
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                                                                                                    Rattus norvegicus (Rat).
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                                                                                                                      Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
VELASCO J.A., FELJOO E., AVILA M.A., NOTARIO V.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: U96612. AAB71812.1; -.
PFAM: PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
NEU DIFFERENTIATION FACTOR NDF38.
                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
NEUREGUIN.
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1437D80A CRC32;
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SEQUENCE 46
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SEQUENCE
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P43323;
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Mol. Cell. Biol. 14:1909-1919(1994).

EMBL; U02338; AAA19953.1;

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SEQUENCE 552 AA; 60845 MW; 3F7DD741 CRC32;
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MEDLINE; 94158863.
WEN D., SUGGS S.V., KARUNAGARAN D., LIU N., CUPPLES R.L., LUO Y.,
JANSSEN A.M., BEN-BARUCH N., TROLLINGER D.B., JACOBSEN V.L.,
MENG S.Y., LU H.S., HU S., CHANG D., YANG W., YANIGAHARA D.,
COSKIR RA., YARDEN Y.;
"Structural and functional aspects of the multiplicity of Neu
differentiation factors.";
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                                                                                                                                                                                                       DB 11; Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-NOV-1998 (TIEMBLIEL. 08, Last annotation update)
NEU DIFFERENTIATION FACTOR (FRAGMENT).
   POTENTIAL.
K -> N (IN REF. 2).
Y -> S (IN REF. 2).
W; CC0E2197 CRC32;
                                                                                                                                                                                                Query Match

40.3%; Score 111.5; DB 1.
Best Local Similarity 34.8%; Pred. No. 2.5e-07;
Matches 16; Conservative 13; Mismatches 16
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   265
90
K
208
¥6309 MW;
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243 2
90
208
422 AA;
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MEDLINE; 94158863.
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TRANSMEM
CONFLICT
CONFLICT
                                                                                                  SEQUENCE
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Q12782;
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012782
AC 012782
AC 012782
DT 01-NOV-
DT 01-N
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012783
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MEDILIRE, 95301541.
HOW H., ARWANIN M.P., NUIJENS A., PHILLIPS H.S., OSHEROFF P.L.;
"Sensory and motor neuron-derived factor. A novel heregulin variant highly expressed in sensory and motor neurons.";
J. Blol. Chem. 270:14523-14532(1995).
EMBL; L41827; AAC41764.1;
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WEDLINE; 94158863.
WED LINE; 94158863.
WEN D., SUGGS S.V., KARUNAGARAN D., LIU N., CUPPLES R.L., LUO JANSSEN A.M., BEN-BARUCH N., TROLLINGER D.B., JACOBSEN V.L., MENG S.Y., LU H.S., HU S., CHANG D., YANG W., YANIGAHARA D., KOSKI R.A., YARDEN Y.;
Structural and functional aspects of the multiplicity of Neu differentiation factors.";
Structural and functional laspects of the multiplicity of Neu differentiation factors.";
EMBL: U02330; AAA19955.1;
PERM: PFO0008; EGF: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.7%; Score 104.5; DB 4; Length 175; Best Local Similarity 31.2%; Pred. No. 9.2e-07; Matches 15; Conservative 14; Mismatches 18; Indels 1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                         Length 288;
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Eutheria; Primates; Catarrhin; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                         1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                                              Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
NEU DIFFERENTIATION FACTOR (FRAGMENT).
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                                                                                                                                                                                                                37.7%; Score 104.5; DB 4;
31.2%; Pred. No. 1.5e-06;
tive 14; Mismatches 18;
EMBL; U02329; AAA19954.1; -.
PFAM; PF00008; EGF; 1.
NON_TER 1 1
NON_TER 288 288
SEQUENCE 288 AA; 31488 MW; 60DF34F9 CRC32;
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
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Best Local Similarity 31.2%
Matches 15; Conservative
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Search completed: October 14, 1999, 00:32:24
Job time: 6461 sec
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-!- TISSUE SPECIFICITY: EXPRESSED IN NERVOUS SYSTEM: SPINAL CORD AND
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 97472144.
SCHARFER G., FITZPATRICK V.D., SLIWKOWSKI M.X.;
"Gamma-heregulin a novel heregulin isoform that is an autocrine growth factor for the human breast cancer cell line, MDA-MB-175.";
Oncogene 15:1385-1394(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 93205115.
MARCHIONNI M.A., GOODEARL A.D., CHEN M., BERMINGHAM-MCDONOGH O., MARCHIONNI M.A., GOODEARL A.D., CHEN M., BERMINGHAM-MCDONOGH O., KIRK C., HENDRICKS M., DANEHY F., MISUHI D., SUDHAITER J., KOBAYASHI K., WROBLENSKI D., LYNCH C., BALDASARRE M., HILES I., DAVIS J.B., HSUAN J., TOTTY N.F., OTSU M., MCBURNEY R.N., WATERFIELD M.D., STROCBANT P., GWYNNE D.; "Gilal growth factors are alternatively spliced erbb2 ligands expressed in the nervous system.";
Nature 362:312-318(1993).
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; Pred. No. 3.9e-06;
14; Mismatches 18; Indels 1;
                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                Length 296;
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                                                                                                                                        233 HLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYV 280
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                                                                                                                       1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQFL 47
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-NOV-1998 (TREMBLREL) 08, Last annotation update)
GLIAL GROWTH FACTOR 2 PRECURSOR (NEUREGULIN) (GGFHPP2).
                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                             Score 104.5; DB 4;
Pred. No. 1.5e-06;
4; Mismatches 18;
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768 AA; 84177 MW; 8D5E27FF CRC32;
                59F09FC6 CRC32;
                                                                                                                                                                                                                                    768 AA
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                                                                                           14;
PFAM; PF00008; EGF; 1.
SEQUENCE 296 AA; 31685 MW;
                                                             37.7%;
31.2%;
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31.2%;
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PFAM; PF00008; EGF; 1.
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Best Local Similarity 31.28
Matches 15; Conservative
                                                           Query Match
Best Local Similarity 31.2%
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                              GAMMA-HEREGULIN.
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SEQUENCE
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Gaps
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                                                                                                                                                                                                                                                            1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQFL
EMBL; L12260; AAF59622.1; --
PROSITE; PS00022: EGF; 1.
PFAM; PF00008; EGF; 1.
PFAM; PF00047; ig; 1.
SIGNAL is 6F-11ke domain; Glycoprotein; Signal.
SIGNAL 1 44
POTENTIAL.
CHAIN 45 422 GLIAL GROWTH FACTOR 2.
                                                                                                                                        Q -> R.
BC6DC7F1 CRC32;
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POLY-ALA.
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39 P
105 P
253 Q
45112 MW;
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Best Local Similarity
Matches 15; Conserva
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45
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101
253
422 AA;
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GenCore version 4.5
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using sw model - protein search, OM protein October 13, 1999, 14:00:21 ; Search time 33.23 Seconds Run on:

(without alignments) 56.668 Million cell updates/sec

US-09-107-979-4
277
1 HFKPCRDKDLAYCLNDGECF.....SHKHCRCKEGYQGVRCDQFL Title: Perfect score: Sequence:

BLOSUM62 Scoring table:

40065486 residues 122810 seqs, Searched:

PIR_60:* Database :

pir1:*
pir2:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	herequlin precurso	neu differentiatio	heregulin isoform	glial growth facto	heregulin precurso	heregulin precurso	heregulin, splice	neu differentiatio	neu differentiatio	neu differentiatio	sensory/motor neur	lia	neu differentiatio	acetylcholine rece	ErbB_kinase activa			()	growth factor - ra	jagged protein pre	epiregulin precurs	epiregulin - rat	gene Notch-1 prote	Notch homolog Motc	betacellulin precu	ctor	probable EGF-like		orming	н									
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SUMMAKIES	ID	A43273	I38404	138405	151716	161719	161724	S62676	S32357	C43273	D43273	B43273	138406	138407	I38408	A56943	S32359	161718	161721	161722	A56210	161720	A45769	JC5700	JC5701	JC5702	PC4417	EGVZSF	A56136	568401	JT0747	A46019	A48825	A37408	EGVZM1	A44074	JC1467	WFRT1	WMVZ9	WMVZ3C
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	ength	640	462	125	461	639	422	125	422	637	241	645	552	288	175	296	241	636	636	662	230	304	602	850	868	860	641	80	1220	162	46	2531	861	177	82	230	178	159	140	142
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transforming growt	transforming growt	notch protein homo	epidermal growth f	DELTA-like 1 - mou	epidermal growth f	
S27195	157497	S18188	EGHU	148324	EGMSMG	
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159	159	2531	1207	722	1217	
28.7	28.7	28.5	28.2.	28.0	27.4	
79.5	79.5	79	78	77.5	9/	
40	41	42	43	44	45	

ALIGNMENTS

Gaps ij Length 640; Indels 15; DB 2; 41.0%; Score 113.5; DB 2 34.8%; Pred. No. 5.6e-06; 14; Mismatches Best Local Similarity 34.8 Matches 16; Conservative Query Match

1;

1 HFKPCRDKDLA/CLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45 δ

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RESULT I38404

neu differentiation factor - human c; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: 19 May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
C; Accession: 138404
R; Wen, D.; Suggs, S.V., Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A. Mol. Cell. Biol. 14, 1909-1919, 1994
A; Title: Structural and functional aspects of the multiplicity of Neu differentiation A; Reference number: A; 56210; MUID: 94158863
A; Reference number: A; 56210; MUID: 94158863
A; Status: preliminary: translated from GB/EMBL/DDBJ

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C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Aug-1998
C; Accession: 161724; A38220
B; Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A. Mol. 14, 1509-1919, 1994
Mol. Cell. Biol. 14, 1509-1919, 1994
A; Title: Structural and functional aspects of the multiplicity of Neu differentiation A; Reference number: A56210; MUID:94158863
A; Accession: 161724
A; Astatus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: MRNA
A; Residues: 1-422 <RESS
          Species: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Aug-1998 (Species: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Aug-1998 (Species: 29-May-1998 #sequence_revision 29-May-1998 #sequence_revision 29-May-1998 #sequence_revision 29-May-1998 #sequence_revision 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 161719; 16171
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R;Wen, D.; Peles, E.; Cupples, R.; Suggs, S.V.; Bacus, S.S.; Luo, Y.; Trail,
Cell 69, 559-572, 1992
A;Title: New differentiation factor: a transmembrane glycoprotein containing
A;Reference number: A38220; MUID:92257596
A;Accession: A38220
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A;Residues: 1-422 <WEN>
A;Note: sequence extracted from NCBI backbone (NCBIN:101767, NCBIP:101768)
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34.8%; Pred. No. 9.5e-06;
iive 13; Mismatches 16;
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34.8%; Pred. No. 6.6e-06;
iive 13; Mismatches 16
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A;Molecule type: mRNA
A;Residues: 1-639 <RE:>
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- rat
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Best Local Similarity 34.8'
Matches 16; Conservative
neu differentiation factor
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Best Local Similarity
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
R;Accession: 1805 1994 #sequence_revision 29-May-1998 #text_change 29-May-1998
Mol. Cell. Biol. 14, 1909-1919, 1994
A;Ritle: Structural and functional aspects of the multiplicity of Neu differentiation fants.
A;Reference number: A56210; WUID:94158863
A;Accession: 138405
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C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Aug-1998
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Aug-1998
C; Accession: 161716; 161717
Mol. Cell. Biol. 14, 1909-1919, 1994
A; Title: Structural and functional aspects of the multiplicity of Neu differentiation fa A; Reference number: A56210; MUID: 94158863
A; Accession: 161716
A; A; Accession: 161716
A; A; Accession: 161716
A; A; Accession: Indianary; translated from GB/EMBL/DDBJ
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A;Cross-references: EMBL:U02316; NID:g408382; PID:g408383
A;Accession: 161717
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A;Residues: 1-461 <FE2>
A;Cross references: EMBL:U02317; NID:g408384; PID:g408385
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A.Molecule type: mRNA
A.Residues: 1-125 <RES>
A;Cross-references: EMBL:U02327; NID:g408404; PID:g408405
                         A;Molecule type: mRNA
A;Residues: 1-462 <RES>
A;Cross-references: EMBL:U02326; NID:9408402; PID:9408403
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Best Local Similarity 34.8%; Pred. No. 7.1e-06;
Matches 16; Conservative 13; Mismatches 16;
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ilarity 34.8%; Pred. No. 1.3e-06;
Conservative 14; Mismatches 15;
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neu differentiation factor - human (fragment)
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Matches 16; Conserv
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Best Local S
Matches 16
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J.W.; Yan

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A.Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A; Molecule type: mRNA
A; Residues: 1-241 <HOLD-
B; Marsidues: 1-241 <HOLD-
B; Marsidues: 1-241 <HOLD-
B; Marchionni, M.A.; Goodearl, A.D.J.; Chen, M.S.; Bermingham-McDonogh, O.; Kirk, C.; Les, I.; Davis, J.B.; Hsuan, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield, Nature 362, 312-318, 1993
A; Feference number: 532357; MUID:993205115
A; Reference number: 532357; MUID:993205115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: B43273
A,Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
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                                                                                                                                                 1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQFL 47
                          HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQFL
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Pred. No. 2.7e-05;
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C; Superfamily: GGF homology
C; Reywords: alternative splicing
F;182-221/Domain: EGF .:omology <EGF>
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Best Local Similarity 31.2%
Matches 15; Conservative
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C:Superfamily: EGF homology
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A; Residues: 1-645 <HOI,>
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C. Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 14-Aug-1998
C. Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 14-Aug-1998
C. Science 256, 1205-1210, 1992
R. Holmes, W.E.; Sliwkwski, M.X.; Akita, R.W.; Henzel, W.J.; Lee, J.; Park, J.W.; Yansur Science 256, 1205-1210, 1992
A. Title: Identification of heregulin, a specific activator of p185(erbB2).
A. Reference number: A43273; MUID:92271253
A. Accession: C43273
A. Accession: C43273
A. Accession: C43273
A. Accession: C43273
A. Residues: 1-637
A. Molecule type: mRNA
A. Residues: 1-637
A. Molecule type: mRNA
A. Residues: 1-637
A. Cross-references: GDB:132656; OMIM:142445
A. Map position: B922-8Bp11
C. Superfamily: EGF homology
C. Keywords: alternative splicing
F. 182-221/Domain: EGF homology <EGF>
A;Title: Isolation and structural characterization of recombinant human neu differentiat
A;Reference number: S62676; MUID:96139341
A;Accession: S62676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S32357
R;Marchionni, M.A.; Goodearl, A.D.J.; Chen, M.S.; Bermingham-McDonogh, O.; Kirk, C.; He les, I.; Davis, J.B.; Hsuan, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield, Mature 362, 312-318, 1993
A;Title: Glial growth factors are alternatively spliced erbB2 ligands expressed in the A;Reference number: S32357; MUID:93205115
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;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
;Accession: 532357
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C;Species: Homo sapiens (man)
C;Date: 31-Dec_1993 #sequence_revision 31-Dec-1993 #text_change 14-Aug-1998
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                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6;7-16;17-30;31-38;39-58;59-92;93-120;121-125
C;Keywords: proto-oncogene
                                                                                                                                                                                                                                                                                                                                                         1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                  38.1%; Score 105.5; DB 2; 32.6%; Pred. No. 1.1e-05; tive 14; Mismatches 16;
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31.2%; Pred. No. 6.2e-05;
tive 14; Mismatches 18
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A; Residues: 1-422 <MAR>
C; Superfamily: EGF homology
F; 363-402/Domain: EGF homology <EGF>
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Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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A; Status: preliminary
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R;Ho, W.H.; Armanini, M.P.; Nuijens, A.; Phillips, H.S.; Osheroff, P.L.
J. Biol. Chem. 270, 14523-14532, 1995
A;Title: Sensory and motor neuron-derived factor. A novel heregulin variant highly ex
A;Reference number: A56943; MUID:95301541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 10-Sep-1997
C;Accession: A56943
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                                                                                                                                                                                                                                                            1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQFL 47
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A;Cross-references: GB:L41827; NID:9862422; PID:9862423
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                               ; Score 104.5; DB 2;
; Pred. No. 2e-05;
14; Mismatches 18;
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me: 12300 sec
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                                    37.7%;
31.2%;
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Best Local Similarity
Matches 15; Conserv
                                    Query Match
Best Local Similarity
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A; Residues: 1-296 <HOA>
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C. Species: Homo sapiens (man)
C. Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
C. Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
C. Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
C. Date: 2
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
C;Date: 29-May-1998 #sequence_revision 29-May-1998
C;Date: 29-May-1998 #sequence_revision 29-May-1998
R;Mconson: 158408
Mol. Cell. Biol. 14, 1909-1919, 1994
Mol. Cell. Biol. 14, 1909-1919, 1994
A;Title: Structural and functional aspects of the multiplicity of Neu differentiation fa
A;Reference number: A56210; MUID:94158863
A;Accession: I38408
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Residues: 1-175 cRES>
A;Cross-references: EMBL:U02330; NID:9408411
                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: 138406

R; Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.; Mol. Cell. Biol. 14, 1909-1919, 1994

A; Title: Structural and functional aspects of the multiplicity of Neu differentiation fa A; Reference number: A56210; MUID:94158863

A; Accession: 138406
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
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                                                 1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQFL 47
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A;Molecule type: mRNA
A;Residues: 1-552 <RES-
A;Cross-references: EMBL:U02328; NID:g408406; PID:g408407
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Gaps

1;

Indels

Length 296;

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM protein - protein search, using sw model

October 14, 1999, 01:54:24 ; Search time 10.23 Seconds (without alignments) 129.874 Million cell updates/sec Run on:

US-09-107-979-4
277
1 HFKPCRDKDLAYCLNDGECF....SHKHCRCKEGYQGVRCDQFL 47

Title: Perfect score: Sequence:

Scoring table: BLOSUM62

77977 seqs, 28268293 residues Searched:

SwissProt_37:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	scription		OHOU	rattus	shop	mus	Q05928 mus musculu	P08072 myxoma viru	Q01083 drosophila	P35070 homo sapien	P20494 vaccinia vi	vaccini	P48030 mus musculu	P01134 rattus norv		рошс	m snm	ratt	P10040 drosophila	snw				cavia		bos t	homo	Q61554 mus musculu	P16581 homo sapien	P27113 oryctolagus	P42287 drosophila	P79385 sus scrofa	xeno	mus m	рошо	snш		P55244 macaca mula		strongy		P98157 gallus gall	P01135 homo sapien	P98138 oryctolagus	Q00968 sus scrofa
SUMMARIES		:	NIAK_HUMAN	NTAK_RAT	GRFA_SFVKA	NTC1_MOUSE	BTC_MOUSE	GRFA_MYXVL	SPIT_DROME	BTC_HUMAN	GRFA_VACCC	GRFA_VACCV	TGFA_MOUSE	TGFA_RAT	NTC1_RAT	EGF_HUMAN	- 1	DLL1_RAT	CRB_DROME	EGF_MOUSE	LEM2_PIG	LEM2_CANFA	DLL1_HUMAN	FA12_CAVPO	LI12_CAEEL	FBN1_BOVIN	FBN1_HUMAN	- 1	LEM2_HUMAN	LEM2_RABIT	GRK_DROME	MFGM_PIG	NOTC_XENLA	NTC4_MOUSE	FA12_HUMAN	HBGF_MOUSE	MFGM_MOUSE	TGFA_MACMU	EGF_RAT		LEM3_MOUSE	LRP1_CHICK	TGFA_HUMAN	الم	EGF_PIG
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HUMAN STANDARD; PR 1, 125.6 2907 1 FENZ 1, 125.6 2908 (REL. 37, LAST SEQUE C-1998 (REL. 37, LAST SEQUE C-1998 (REL. 37, LAST SEQUE C-1998 (REL. 37, LAST ANNOT END SERVING (RUMAN). SAPIENS (HUMAN). TES; CATARRHINI; HOMINIDAE; NEW 1, MATSUS MAN 1. MATSUS	IUMAN P35556 homo sapien OUSE Q61555 mus musculu	ALIGNMENTS	PRT; 850 AA. SEQUENCE UPDATE) SEQUENCE UPDATE) HINUS- DERIVED ACTIVATOR FOR ERBB KINASES). A; VERTEBRATA; MAMMALIA; BUTHERIA; IIDAE; HOMO. ATSUSHITA N., NAGATSU T., TANIGUCHI N., Per of the epidermal growth factor family ING ENDB4."; BB3 AND ERBA TYROSINE KINASE RECEPTORS. EGF-LIKE DOMAIN. POTENTIAL. TO HEPARIN-BINDING PROTEINS. POTENTIAL. There are no restrictions on its Unions as is content is in no way is not removed. Usage by and for commercial is acrement (See http://www.isb-sib.ch/announce/ is not removed. Usage by and for commercial is acrement (See http://www.isb-sib.ch/announce/ is stricker. BY SIMILARITY. BY SIMILARI	d. No. 0.0016; Mismatches 17; Indels 2; Gaps 1;
Land	911	ALIC .	ARD; PRT; 85 CREATED) LIAST SEQUENCE UPPL LIAST ANNOTATION U CHORDATA; VERTEBRAT CHORDATA; CHORDAT CHORDATA; CHORDAT CHORDATA; CHORDAT CHORDATA	9%; Pre 9;
LL 1 (HUMAN) O14511, O14511, O14511, O14511, O15511,	25.6 25.6		STAND STAND 998 (REL. 37 980 (R	Similarity 5; Consérva
	5 7		RESULT INTAK_HUMAN INTAK_HUMAN NITAK_HUMAN NITAK_HUMAN OT 15-DEC-19 DE NITAK_HUMAN SECONDER REAN NITAK_HUMAN NITAK_HUMAN NITAK_HUMAN NITAK_HUMAN NITAK_HUMAN REAN REA	Best Local S Matches 15

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414
868 AA;
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                                                                                                                                                                                                                                             GROWTH FACTOR.
                                                                                                                                                                                                 GRFA_SFVKA
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SEQUENCE
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GRFA_SFVKA
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SOLUTION
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                                                               NTAK_RAT STANDARD; PRT; 868 AA.
035569; 035570; 035571; 035572;
15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
NTAK PROTEIN PRECURSOR (NEURAL- AND THYMUS- DERIVED ACTIVATOR FOR ERBB
                                                                                                                                                                                                                -i - SIMILARITY: BELONGS TO EGF FAMILY. TO HEPARIN BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ig; 1.
;; EGF-LIKE DOMAIN; IMMUNOGLOBULIN FOLD; GLYCOPROTEIN;
                                                                                                                                                                                         HIGASHIYAMA S., HORIKAWA M., YAMADA K., ICHINO N., NAKANO N., NAKAGAWA T., MIYAGAWA J., MATSUSHITA N., NAGATSU T., TANIGUCHI N.,
                                                                                                                                                                       SEQUENCE FROM N.A., SEQUENCE OF 128-162, AND ALTERNATIVE SPLICING
                                                                                                                                    EUKARTUS NORVEGICUS (RAT).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
NTAK PROTEIN.
POTENTIAL.
IG-LIKE C2-TYPE DOMAIN.
EGF-LIKE.
             1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRC 43
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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

POLY-SER.
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POLY-ALA.
POLY-PRO.
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POTENTIAL.
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EMBL; D89996; D1024224; --
EMBL; D89997; D1024225; --
EMBL; D89998; D1024226; --
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                C2-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00008; EGF;
                                                                                                                                                                                    MEDLINE; 98006324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00047
                                                                                                                                                                                                               ISHIGURO H.
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CARBOHYD
CARBOHYD
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                                                                                                                      KINASES).
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                                                                                                       C -> G (IN ISOFORM NTAK-GAMMA).
MISSING (IN ISOFORM NTAK-GAMMA).
NGFFGQRCLEKLPLRLYMPDDFKQKHLGFELKE -> VGYTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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VIRUSES; DSDNA VIRUSES, NO RNA STAGE; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                                                                                                                        DRCQOFAMVNESK (IN ISOFORM NTAK-BETA).
MISSING (IN ISOFORM NTAK-ALPHA2A).
C202303C CRC32;
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Pred. No. 0.0017; 
9; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 80;
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| EGF-LIKE DOMAIN | GROWTH FACTOR; | GLYCOPROTEIN. |
| DOMAIN | 29 | 73 | EGF-LIKE. |
| DISULFID | 33 | 47 | BY SIMILARITY. |
| DISULFID | 41 | 61 | BY SIMILARITY. |
| DISULFID | 63 | 72 | BY SIMILARITY. |
| TARBOHYD | 44 | 44 | POTENTIAL. |
| FORTHER | FORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 85; DB 1;
Pred. No. 0.00077;
5; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1988 (REL. 08, CREATED)
01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB4DA12B CRC32;
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                                 POTENTIAL. POTENTIAL.
POTENTIAL.
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PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG.
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39.2%;
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Best Local Similarity 39.2
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                               93776
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.5
Best Local Similarity 34.9
Matches 15; Conservative
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294
362
388
868
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REPEAT
REPEAT
REPEAT
CARBOHYD
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BTC_MOUSE
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                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                         COPELAND NG., GRIDLEY T.; ORIGINAL PROPERTY CONTROL NO. 1 DENKINS N.A., "CLONING, analysis, and chromosomal localization of Notch-1, a mouse homolog of Drosophila Notch-";
             MTCL_MOUSE STANDARD; PRT; 2531 AA.

101705:
01-104-1995 (REL. 32, CREATED)
01-FEB-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NUDROGENIC LOCUS NOTCH HOWOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN).
NUTCH1 OR MUSCHALS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIFFERENTIATION; NEUROGENESIS; REPEAT; ANK REPEAT; EGF-LIKE DOMAIN; TRANSMEMBRANE; SIGNAL; GLYCOPROTEIN.
SIGNAL
                                                                                                                                   MEDLINE; 93194170.
FRANCO DEL AMO F., GENDRON-MAGUIRE M., SWIATEK P.J., JENKINS N.A.,
COPELAND N.G., GRIDLEY T.;
                                                                                                                                                                                                                                              GREENSPAN R.J., MCMAHON A.P., GRIDLEY T., "Expression pattern of Motch, a mouse homolog of Drosophila Notch, suggests an important role in early postimplantation mouse
                                                                                                                                                                                                                                        FRANCO DEL AMO F., SMITH D.E., SWIATEK P.J., GENDRON-MAGUIRE M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL). 36 X EGF-TYPE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIN/NOTCH 1.
LIN/NOTCH 2.
LIN/NOTCH 3.
E X ANK MOTIF REPEATS.
ANK MOTIF 1.
ANK MOTIF 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 X LIN/NOTCH REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:97363; NOTCHI.
PROSITE; PS00010; ASX HYDROXYL; 22.
PROSITE; PS00010; ASX HYDROXYL; 22.
PROSITE; PS01186; EGF_2: 27.
PROSITE; PS01187; EGF_CA: 21.
PFAM; PF00008; EGF: 35.
PFAM; PF00008; ABF: 6.
PFAM; PF00006; notch; 3.
HSSP; P00740; 11XA.
                                                                                                                                                                                                           SEQUENCE OF 1551-2170 FROM N.A.
                                                                                                                                                                                         GENOMICS 15:259-264(1993).
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1522
1562
                                                                                                                                                                                                                     TISSUE=EMBRYO;
MEDLINE; 93048835.
                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                TISSUE=EMBRYO;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GROWTH FACTOR; MITOGEN; GLYCOPROTEIN; EGF-LIKE DOMAIN; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PRECURSOR FORM);
EXTRACELLULAR (MATURE FORM).
-!- TISSUE SPECIFICITY: FOUND IN SEVERAL MOUSE TISSUES INCLUDING
KIDNEY, UTERGY AND LIYER AS WELL AS IN BETA TUMOR CELL LINE AND
MCF-7 CELLS. IT IS NOT DETECTED IN THE BRAIN.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: STRONG, TO HUMAN BETACELLULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: POTENT MITGEN FOR RETINAL PIGMENT EPITHELIAL CELLS AND VASCULAR SMOOTH MUSCLE CELLS. THE EFFECTS OF BETACELLULIN ARE PROBABLY MEDIATED BY THE EGF RECEPTOR AND OTHER RELATED
                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHING Y., CHRISTOFORI G., HANAHAN D., ONO Y., SASADA R., IGARKARI K., FOLKMAN D.; Betacallulin: a mitogen from pancreatic beta cell tumors."; SCIENCE 259:1604-1607(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 32-54; 64-71 AND 75-111.
TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                    Score 83; DB 1; Length 2531;
Pred. No. 0.03;
4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BETACELLULIN.
REMOVED IN MATURE FORM.
                                                                                                                                                                                                                   AD71189B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                1064 DSAPCKNGGRCW----QTNTQYHCECRSGWTGVNCD 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28, CREATED)
28, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                     9 DLAYCLNDGECEVIETLTGSHKHCRCKEGYQGVRCD 44
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ANK MOTIF ANK MOTIF ANK MOTIF POTENTIAL.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR, A37408, A37408.
MGD; MGI:99439; ETC.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PFAM; PF00008; EST; 1.
HSSP; P01135; 1YUF.
                                                                                                                                                                                                                                                                                      Query Match 30.0%;
Best Local Similarity 41.7%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L08394; G293853; -.
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2009
2042
2075
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1587
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MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                        ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (REL. 01-FEB-1994 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93206093
                                                                                            959
11179
1241
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2531
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112
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Q05928;
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                                                                                                                                                                                                    Gaps
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PUPPON C., MACEN J.L., MCFADDEN G.;

"Mapping and sequencing of a gene from myxoma virus that is related to those encoding epidermal growth factor and transforming growth
                                                                                                                                                                                                                                                                                                                                       01-AUG-1988 (REL. 08, CREATED)
01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
GROWTH FACTOR (MGF).
MYXOMA VIRUS (STRAIN LAUSANNE).
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 91182748.
LIN Y.-Z., KE X.-H., TAM J.P.;
"Synthesis and structure-activity study of myxoma virus growth
                                                                                                                                                                                                      ŝ
                                                                                                                                                                          29.8%; Score 82.5; DB 1; Length 177; 39.1%; Pred. No. 0.0031;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                            1 HFKPCRDKDLAYCLNDGEC-FVIETLTGSHKHCRCKEGYQGVRCDQ 45
             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                    14;
                                                                                                                                        B2A6D489 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00008; EGF; 1.
EGF-LIKE DOMAIN; GROWTH FACTOR; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
19584804 CRC32;
                                                           POTENTIAL.
POTENTIAL.
EGF-LIKE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                      9; Mismatches
                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOCHEMISTRY 30:3310-3314(1991)
                                                                                                                                         19664 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor alpha.";
J. virol. 61:1271-1275(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW.
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M15806; G332300; -
                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNTHESIS, AND ACTIVITY.
  1118
1139
1153
1153
1153
105
105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGVZM3
                                                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    LEPORIPOXVIRUS.
                                                                                                                                                                                                                                                                                                                  GRFA_MYXVL
P08072;
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CARBOHYD
SEQUENCE
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DISULFID
SEQUENCE
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DOMAIN
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DOMAIN
                                                                CARBOHYD
                                                   CARBOHYD
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                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila eye where it interacts with the EGF receptor."

MECH. DEV. 48:25-33(1994).

-!- FUNCTION: PROBABLE LIGAND THAT IS BOUND BY THE RECEPTOR TOP.

INVOLVED IN A NUMBER OF URRELATED DEVELOPMENTAL CHOICES, FOR EXAMPLE, DORSAL-VENTRAL AXIS FORMATION, GLIAL MIGRATION, SENSORY ORGAN DETERMINATION, AND MUSCE DEVELOPMENT. IT IS REQUIRED FOR PHOTORECEPTOR DETERMINATION.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 92354912.
RUTLEDGE B.J., ZHANG K., BIER E., JAN Y.N., PERRIMON N.;
"The Drosophila spitz gene encodes a putative EGF-like growth factor involved in dorsal-ventral axis formation and neurogenesis.";
GENES DEV. 6:1503-1517(1992).
                                          Gaps
                                           ;;
                                                                                                                                                                                                                                                                                       EUKARYOTA; MITAZOA; ARTHROPODA; TRÁCHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEUROGENESIS; DEVELOPMENTAL PROTEIN; TRANSMEMBRANE; SIGNAL;
GLYCOPROTEIN; EGF-LIKE DOMAIN.
Score 82; DB 1; Length bu, Pred. No. 0.0019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i-SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i-TISSUE SPECIFICITY: EXPRESSED THROUGHOUT THE EMBRYO.
-i-SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN SPITZ.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                         3 KPCRDKDLAYCLNDGECFVIETLTGS-HKHCRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                       (REL. 32, CREATED)
(REL. 32, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-LIKE.
POLY-ASP.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                          230 AA
                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                              DROSOPHILA MELANOGASTER (FRUIT FLY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, M95199; G158455; -.
FLYBASE; FBGN0005672; spi.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PFAM; PF00008; EGF; 1.
HSSP; P01132; 1EPH.
               29.6%;
                                             Conservative
                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                   PROTEIN SPITZ PRECURSOR.
                Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95134691.
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18
140
161
61
74
78
78
108
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SIGNAL
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01-NOV-1995 (
01-OCT-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FREEMAN M.;
                                                                                                                                                                            SPIT_DROME Q01083;
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DISULFID
DISULFID
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION.
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GRFA_VACCC
P20494;
 DISULFID
DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Matches
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GROWIH FACTOR; MITOGEN; GLYCOPROTEIN; EGF-LIKE DOMAIN; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PRECURSOR FORM); EXTRACELLULAR (MATURE FORM).
TISSUE SPECIFICITY: SYNTHESIZED IN SEVERAL TISSUES AND TUMOR CELLS. PROBABLY NOT FOUND IN THE BRAIN.
                                                                                                                                                                                                                                                                                                                                           SASADA R., ONO Y., TANIYAMA Y., SHING Y., FOLKWAN J., IGARASHI K.; "Cloning and expression of cDNA encoding human betacellulin, a new member of the EGF family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- DISEASE: BETACELLULIN FROM BETA CELLS COULD PLAY A ROLE IN THE VASCULAR COMPLICATIONS ASSOCIATED WITH DIABETES.
-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i- SIMILARITY: STRONG, TO MOUSE BETACELLULIN.
                                                                                                                                                                                                                                                                                                                                                                           BIOCHEM. BIOPHYS. RES. COMMUN. 190:1173-1179(1993).
-!- FUNCTION: POTENT MITGER FOR RETINAL PIGMENT EPITHELIAL CELLS
- RAD VASCULAR SMOOTH MUSCLE CELLS. THE EFFECTS OF BETACELLULIN
ARE PROBABLY MEDIATED BY THE EGF RECEPTOR AND OTHER RELATED
                                                                     ;
0
                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                          Query Match 29.6%; Score 82; DB 1; Length 230; Best Local Similarity 38.9%; Pred. No. 0.0045; Matches 14; Conservative 4; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BETACELLULIN.
REMOVED IN MATURE FORM.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
ARG/LYS-RICH (BASIC).
POTENTIAL.
EGF-LIKE.
BY SIMILARITY.
 POTENTIAL.
23E12DD2 CRC32;
                                                                                                           83 DAWYCLNDAHCFAVKIADLPVYSCECAIGFMGQRCE 118
                                                                                                                                                                                                01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                           9 DLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCD 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
 70 Pr
25967 MW;
                                                                                                                                                                                                                                  BETACELLULIN PRECURSOR (BTC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00022; EGE_1; 1. PROSITE: PS01186; EGE_2; 1. PFAM: PF00008; EGF; 1. HSSP; P01135; 1YUF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S55606; G265786; -. PIR; JC1467, JC1467. MIM; 600345; -.
                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31
178
1178
1139
178
154
105
                                                                                                                                                                                                                                                           SAPIENS (HUMAN).
            230 AA;
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=BREAST;
MEDLINE; 93176165.
                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTORS
                                                                                                                                                                          BTC_HUMAN
P35070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
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DISULFID
            SEQUENCE
  CARBOHYD
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CHAIN
PROPEP
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                                                                                                                                                    RESULT
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                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     VACCINIA VIRUS (STRAIN COPENHAGEN).
VIRUSES: DSDNA YIRUSES, NO RNA STAGE; POXVIRIDAE; CHORDOPOXVIRINAE;
ORTHOPOXVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 91021027.
GOEBEL S.U., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.,
PAOLETII E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOEBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P., PAOLETII E.;
VIROLOGY 179:S17-563(1990).
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                     ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä,
                                                                                               Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 142;
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                 45
                                                                                                                                                                           1 HFKPCRDKDLAYCLNDGEC-FVIETLTGSHKHCRCKEGYQGVRCDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 79.5; DB 1;
Pred. No. 0.0058;
6; Mismatches 15;
                                                                                           29.1%; Score 80.5; DB 1;
illarity 41.3%; Pred. No. 0.0054;
Conservative 5; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete DNA sequence of vaccinia virus."; VIROLOGY 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 CRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7B8CE6B0 CRC32;
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DOMAIN 41 81 EGF-LIKE.

DISULLID 45 58 BY SIMILARITY.

DISULLID 53 69 BY SIMILARITY.

DISULLID 71 80 BY SIMILARITY.

A 34 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                             142 AA
 BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                               PRT;
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93 BY
104 BY
19746 MW;
                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQI
01-FEB-1996 (REL. 33, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MM;
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Local Similarity 38.5%;
Nes 15; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS(0022; EGF_1; 1. PROSITE; PS01186; EGF_2; 1.
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58
69
80
34
95
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                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00008; EGF; 1.
HSSP; P01132; 1EPH.
77
95 1
178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; C42503; WMVZ3C
                                                                                           Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41
45
53
71
34
95
142 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                             GROWTH FACTOR.
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BIOCHIM. BIOPHYS: ACTA 1132:322-324(1992)
                                                                             MEDLINE; 97031181
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159 A
                                                                                                                                       LUETTEKE N.C.;
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TRANSMEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
TRANSFORMING GROWTH FACTOR ALPHA PRECURSOR (TGF-ALPHA) (EGF-LIKE TGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                       VENKATESAN S., GERSHOWITZ A., MOSS B.; "Complete nucleotide sequences of two adjacent early vaccinia virus genes located within the inverted terminal repetition.";
                                                                                                                                                                       VACCINIA VIRUS (STRAIN WR).
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAUGHAN T.J., PASCALL J.C., BROWN K.D.;
"Nucleotide sequence and tissue distribution of mouse transforming growth factor-alpha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             э;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAMMALIA; EUTHERIA;
MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.7%; Score 79.5; DB 1; Length 140; Best Local Similarity 38.5%; Pred. No. 0.0058; Matches 15; Conservative 6; Mismatches 15; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EB38774D CRC32;
                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GROWTH FACTOR; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-LIKE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                       140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 AA
                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA, CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J02421; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15524 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A01391; WMVZ9.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                 VIROL. 44:637-646(1982)
                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
69
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00008; EGF; 1.
HSSP; P01132; 1EPH.
                                                                         21-JUL-1986 (REL. 01,
21-JUL-1986 (REL. 01,
01-FEB-1996 (REL. 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ETGF) (TGF TYPE 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE, 93041937.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       83059924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-LIKE DOMAIN;
                                                                                                                                 GROWTH FACTOR.
                                                                                                                                                                                                             ORTHOPOXVIRUS
                                     GRFA_VACCV
P01136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGFA_MOUSE
P48030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
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                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
RESULT 10
GRFA_VACCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGFA_MOUSE
TGFA_MOUSE
TGFA_M
AC 04(808)
DT 01-FEB
DT 01-FEB
DT 01-FEB
DE (ETGF)
GN TGFA.
GN TGFA.
CC ROBENT
RN [1]
RN [1]
RR SEDUEN
RX MEDLIN
RA VAUGHA
RT GRACE
RT GRACE
RT GRACE
RT GRACE
RAGHA
RA VAUGHA
RT GRACE
RT GRA
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                                                                                                                                 TGFA_RAT STANDARD; PRT; 159 AA.
P01134; 063749;
21-UUL-1986 (REL. 01, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-TUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
(ETANSFORMING GROWTH FACTOR ALPHA PRECURSOR (TGF-ALPHA) (EGF-LIKE TGF)
(ETGF) (TGF TYPE 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                  BERKOWITZ E.A., SEROOGY K.B., SCHROEDER J.A., RUSSELL W.E., EVANS E.P., RIEDEL R.F., PHILLIPS H.K., HARRISON C.A., LEE D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REMOVED IN THE MATURE FORM.
TRANSPORMING GROWTH FACTOR ALPHA.
REMOVED IN MATURE FORM.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 79.5; DB 1; Length 159; Pred. No. 0.0065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P01135; 1YUF.
GROWTH FACTOR; TRANSFORMING PROTEIN; MITOGEN; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
EGF-LIKE
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FFFF9A37 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-LIKE DOMAIN; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.7%;
37.8%;
SEQUENCE FROM N.A.
STRAIN=129/SV; TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:98724; TGFA.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M92420; G202156; --
EMBL; U65016; G1518851; --
EMBL; U64873; G1518849; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
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Best Local Similarity
Matches 17; Conserv
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'n

3;

Gaps

5,

Indels

17;

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Matches
                                                                                                      RESULT 1
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                              δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                 J. BIOL. CHEM. 258:13606-13613(1983).
-!- FUNCTION: TGF ALPHA IS A MITOČENIC POLYPEPTIDE THAT IS ABLE TO
BIND TO THE EGF RECEPTOR AND TO ACT SYNERGISTICALLY WITH TGF BETA
TO PROMOTE ANCHORAGE-INDEPENDENT CELL PROLIFERATION IN SOFT AGAR.
-!- SUBECELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PRECURSOR FORM);
EXTRACELLULAR (MATURE FORM).
-!- SIMILARITY: CONTAINS I BGF-LIKE DOMAIN.
            SEQUENCE FROM N.A.
MEDLINE; 85111164.
LEE D.C., ROSE T.M., WEBB N.R., TODARO G.J.;
"Cloning and sequence analysis of a cDNA for rat transforming growth
                                                                                                                                            BLASBAND A.J., ROGERS K.T., CHEN X., AZIZKHAN J.C., LEE D.C.; "Characterization of the rat transforming growth factor alpha gene and identification of promoter sequences."; MOL. CELL. BIOL. 10:2111-2121(1990).
                                                                                                                                                                                                                                               MARQUARDT H., HUNKAPILLER M.W., HOOD L.E., TODARO G.J.;
"Rat transforming growth factor type 1: structure and relation to epidermal growth factor.";
SCIENCE 223:1079-1082(1984).
                                                                                                                                                                                                                                                                                                                                                                                      Isolation, chemical characterization, and potentiation by other transforming factors from feline sarcoma virus-transformed rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REMOVED IN THE MATURE FORM.
TRANSFORMING GROWTH FACTOR ALPHA.
REMOVED IN MATURE FORM.
                                                                                                                                                                                                                                                                                                                                                                       Epidermal growth factor-like transforming growth factor. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P01135; 1YUF.
GROWTH FACTOR; TRANSFORMING PROTEIN; MITOGEN; GLYCOPROTEIN;
EGF-LIKE DOMAIN; TRANSMEMBRANE; SIGNAL.
1 23 POTENTIAL.
1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
EGF-LIKE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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F1206255 CRC32;
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EMBL; M31075; G554526; -.
EMBL; M31076; G207282; -.
PIR; A01389; WFRT1.
PROSITE: PS00022; EGF_1; 1.
PROSITE: PS01186; EGF_2; 1.
                                                                                     NATURE 313:489-491(1985).
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HSSP; P01135; 1YUF
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25
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159 AA;
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MEDLINE; 84061765.
MASSAGUE J.;
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                       SEQUENCE OF 39-88
                                                                                                                                                                                                                                      MEDLINE; 84121322
                                                                                                                                   MEDLINE; 90220597
                                                                         factor-alpha.
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EGF-LIKE 2.
EGF-LIKE 4.
EGF-LIKE 4.
EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 10.
EGF-LIKE 11.
CALCIUM-BINDING (POTENTIAL).
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IN THE
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PROSITE; PS00010; ASX_HYDROXYL; 22.
PROSITE; PS00102; EGF_1; 35.
PROSITE; PS01186; EGF_2; 26.
PROSITE; PS01187; EGF_CA; 21.
PFAM; PF00008; EGF; 35.
PFAM; PF00066; notch; 3.
HSSP; P00740; 11XA.
DIFFERRUTIATION; NEUROGENESIS; REPEAT; ANK REPEAT; EGF_LIKE DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENT 113:199-205(1991).
-!- FUNCTION: REQUIRED FOR THE CORRECT DIFFERENTIATION OF A NUMBER
                                                                                                                                                                                                                                                                                                                                                     RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGHEST LEVELS OCCUR
DAYS 12 AND 14 AND DECREASE RAPIDLY TO MUCH LOWER LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEINMASTER G., ROBERTS V.J., LEMKE'G.;
"A homolog of Drosophila Notch expressed during mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
1 HFKPCRDKDLAYCLNDGEC-FVIETLTGSHKHCRCKEGYQGVRCD 44
                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS. SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS. SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                      NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.
                                                                                                                                                                                                                           (REL. 32, CREATED)
(REL. 32, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                              PRT; 2531 AA
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15-JUL-1998 (
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Q07008;
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CALCIUM-BINDING (POTENTIAL)

Score 79.5; DB 1; Length 159; Pred. No. 0.0065;

28.7%; 37.8%;

Query Match Best Local Similarity

		Indels 4; Gaps
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CALCIUM-BINDING (POTENTIAL).		,
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EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
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            DELTA-LIKE PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                    SIGNAL; EGF-LIKE DOMAIN; GLYCOPROTEIN; TRANSMEMBRANE. SIGNAL 1 17 POTENTIAL
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STRAIN=BALB/C X C57BL/6; TISSUE=EMBRYO;
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PROSITE; PS00010; ASX_HYDROXYL; 3.
PROSITE; PS01022; EGF_1; 8.
PROSITE; PS01186; EGF_2; 8.
PROSITE; PS01187; EGF_C3; 2.
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HSSP; P00740; lIXA.
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CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9.
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    EPIDERMAL GROWTH FACTOR (UROGASTRONE).
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EUKARYOTA; METAZGA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIURCSNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.2%; Score 78; DB 1; Length 1207; 50.0%; Pred. No. 0.06;
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B762FD23 CRC32;
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DELTA-LIKE PROTEIN 1 PRECURSOR (DELTA1).
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les 16; Conservative
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                                                                                                                                            318
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DLL1_MOUSE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
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PFAM: PF000058; Idl_recept_b; 6.
HSSP: P01137; IEPH.
EGF-LIKE DOMAIN: REPEAT; GROWTH FACTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; POLYMORPHISM.
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 83391964.
FURUYA M., AKASHI S., HIRAYAMA K.;
"The primary structure of human EGF produced by genetic engineering, studied by high-performance tandem mass spectrometry.";
BIOCHEM. BIOPHYS. RES. COMMUN. 163:1100-1106(1989).
                                                                                                                                                                                             TISSUE-KIDNEY;
MEDLINE; 87066721.
BELL G.I., FONG N.M., STEMPIEN M.M., WORMSTED M.A., CAPUT D.,
KU L., URDEA M.S., RALL L.B., SANCHEZ-PESCADOR R.;
"Human epidermal growth factor precursor: cDNA sequence, expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE: 92395667.

HOMMEL U., HARVEY T.S., DRISCOLL P.C., CAMPBELL I.D.;

Human epidermal growth factor. High resolution solution structure and comparison with human transforming growth factor alpha.";

J. MOL. BIOL. 227:271-282(1992).

I. FUNCTION: THE GROWTH FACTOR STIMULATES THE GROWTH OF VARIOUS EPIDERMAL AND EPITHELIAL TISSUES IN VIVO AND IN VITRO AND OF SC FIBNOBLASTS IN CELL CULTURE.

I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

I. SUBCELLULAR LOCATION: TYPE I MEMBRANE.
                                                   21-JUL-1986 (REL. 01, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
EPIDERMAL GROWTH FACTOR PRECURSOR, KIDNEY (EGF) (UROGASTRONE).
                                                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPIDERMAL GROWTH FACTOR.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                           SEQUENCE OF 971-1023.
MEDLINE; 77117897.
GREGORY H., PRESTON B.M.;
"The primary structure of human urogastrone.";
INT. J. PEPT. PROTEIN RES. 9:107-118(1977).
                             PRT; 1207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                     in vitro and gene organization.";
NUCLEIC ACIDS RES. 14:8427-8446(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, X04571, G31121; -.
PIR: A25531; EGHU.
MIM; 131530; -.
MIM; 121810; -.
PROSITE; PS000010; ASX_HXDROXYL; 3.
PROSITE; PS01012; EGF_1; 1.
PROSITE; PS01186; EGF_2; 7.
PROSITE; PS01186; EGF_2; 7.
                           STANDARD;
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1207
1032
1053
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 971-1023.
                                                                                                                          HOMO SAPIENS (HUMAN)
                                                                                                                                                                                   SEQUENCE FROM N.A.
RESULT 14
EGF_HUMAN
ID EGF_HUMAN
AC P01133;
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TWIERFERENCE

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

 protein search, using sw model OM protein October 14, 1999, 00:32:25; Search time 10:18 Seconds (without alignments) 52.765 Million cell updates/sec Run on:

US-09-107-979-4 Title: Perfect score:

277
1 HFKPCRDKDLAYCLNDGECF.....SHKHCRCKEGYQGVRCDQFL 47 Sequence:

Scoring table: BLOSUM62

Searched:

Database :

119832 seqs, 11428610 residues

Issued_Patents_AA:*>
1:--/egn2-6/ptodaTe3/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata4/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata4/1/iaa/PCTU59_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		pescription		equence 1,	7	φ,	10,	13,	14,	Sequence 26, Appl	111	ω	10,	13,	e 14,	26,	e 3,	'n	equence 11,	12,	ὼ	10,	equence 13,	14,	equence 26,	11,	equence 12,	11,	12,	ω,	8	10,	13,	equence 14,	26,	110	152	equence 152	equence 39,	α	Sequence 152, App
	ď.	at a second	-4	-08-760-815	-08-761-038-	-847-743B	-07-847-743B-1	-07-847-743B-1	-07-847-743B-1	-07-847-743B	-08-179-481-11	8-456-	-08-456-201-	-08-456-201-1	-08-456-20	-08-456-201-2	-08-417-640A-	8-760-815-3	-08-330-16	-08-330-161-1	.08-456-241-8	8-456-241-1	-08-456-241-1	5-08-456-241-1	S-08-456-241-2	S-08-440-401-1	-08-440-401-1	-419-878B	-08-419-878B-1		04295A-8	04295A-1	04295A-1	04295A-1	8	7	Ψ,	S-08-469-5	-091A-39	S-08-249-3	9-526A-15
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Sequence 152, App Sequence 152, App Sequence 148, App Sequence 152, App Sequence 40, Appli Sequence 5, Appli
US-08-734-591A-152 US-08-469-660-152 PCT-US94-050830-148 PCT-US95-06846A-152 US-08-168-091A-40 US-08-417-640A-5
113335
50 50 50 44 50 60 60 60 60 60 60 60 60 60 60 60 60 60
777788 888688 888688
108.5 108.5 108.5 108.5 107.5
44 44 44 54 44

ALIGNMENTS

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NU!BER: US/08/417,640A
                                                                                          APPLICANT: Carnahan, Josette F. APPLICANT: Hara, Shinichi APPLICANT: Lu, Hsieng S. APPLICANT: Mayer, John P. APPLICANT: Moshinaga, Steven K. TITLE OF INVENTION: NDF Peptides NUMBER OF SEQUENCES: 6 CORRESPONDENCE AMORES: ADDRESSE: AMORE INC.
                                                                                                                                                                                                                                      STREET: 1840 Dehavilland Drive CITY: Thousand Oaks
                                    ; Sequence 1; Application US/08417640A
; Patent No. 5670342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: MAZZA, RICHARD J.
REFERENCE/DOCKJI NUMBER: A
INFORMATION FOR SEQ. ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       ZIP: 91320
RESULT 1
US-08-417-640A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-417-640A-1
                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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1; Query Match
42.1%; Score 116.5; DB 1; Length 52;
Best Local Similarity 33.3%; Pred. No. 9.8e-08;
Matches 16; Conservative 15; Mismatches 16; Indels

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Gaps

1 HFKPCRDKDLA"CLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQFL 47 APPLICANT: Hara, Shinichi
APPLICANT: Lu, Hsieng S.
APPLICANT: Mayer, John P.
APPLICANT: Yoshinaga, Steven K.
TITLE OF INVENTION: NOF Peptides
NUMBER OF SEQUENCES: 6 Sequence I, Application US/08760815; Patent No. 56864.5; GENERAL INFORMATION. Carnahan, Josette F. APPLICANT: US-08-760-815-1 RESULT ò g

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Gaps
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Pred. No. 3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Structure, Production and Use of
TITLE OF INVENTION: Herequlin
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 HLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCQNYV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                                                                                                                                                                      42.1%; Score 116.5; DB 2
33.3%; Pred. No. 9.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION 1 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-May-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-No. 5367060-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hensley, Max D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/847,743B
FILING DATE: 19920306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-847-743B-8; Sequence 8, Application US/07847743B; Patent No. 5367060
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REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,266,1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 669 amino acids TYPE: AMINO ACID
                          NAME: Mazza, Richard J.
REPERBNEALEZH UUMBER:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 33.3%
Matches 16; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                        52 amino acids
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                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-761-038-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                         amino acid
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                                                                                                                                                                                            COUNTRY: VOLUTION COUNTRY: VOLUTION COUNTRY: VOLUTION STATEMENT PROBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/760,815
FILING DATE: 05-DEC-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/417,640
FILING DATE: 06-APR-1955
FILING DATE: 06-APR-1955
ATTONNEY/AGENT INFORMATION:
NAME: MAZZA, Richard J.
REPERBNCE/DOCKET NUMBER: A-310
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TUND: ABBLICATION OF SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
TUND: ABBLICATION OF SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
TUND: ABBLICATION OF SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
TUND: ABBLICATION OF SED ID NO: 1:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 42.1%; Score 116.5; DB 1; Best Local Similarity 33.3%; Pred. No. 9.8e-08; Matches 16; Conservative 15; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/761,038
FILING DATE: 05-DEC-1996
...JUKESS:
STREFF: Amgen Inc.
STREFF: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: Angen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Carnahan, Josette F. APPLICANT: Hara, Shinichi APPLICANT: Lu, Hsieng S. APPLICANT: Mayer, John P. APPLICANT: Yoshinaga, Steven K. TITLE OF INVENTION: NDF Peptides NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/417,640
FILING DATE: 06-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08761038 Patent No. 5929032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-761-038-1
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NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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INFORMATION FOR EQ. ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                        94080
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Gaps
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15; Indels
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                                                          1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                 US-07-847-743B-10
Sequence 10, Application US/07847743B
Sequence 10, S96706
Patent No. 536706
Patent No. 536706
Patent No. 516708
PAPLICANT: Genentech, Inc.
TITLE OF INVENTION: Structure, Production and Use of TITLE OF INVENTION: Herequiin
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Structure, Production and Use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/847,743B
FILING DATE: 19920306
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 41.0%; Score 113.5; DB i
Best Local Similarity 34.8%; Pred. No. 2.8e-07;
Matches 16; Conservative 14; Mismatches 15
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION: 424.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-May 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
FILING DATE: 25-Sep-1991
PRIOR APPLICATION NUMBER: 07/790801
FILING DATE: 08-No. 5367060-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/07847743B Patent No. 5367060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 71:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 10:
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hensley, Max D. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-07-847-743B-10
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US-07-847-743B-13
16;
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Matches
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| Sequence 14, Application US/07847743B
| Sequence 14, Application US/07847743B
| Patent No. 5587060
| GENERAL INFORMATION:
| TILE OF INVENTION: Structure, Production and Use of TITLE OF INVENTION: Heregulin NUMBER OF SEQUENCES: 30
| CORRESPONDENCE ADDRESS: STREET: 460 Point San Bruno Blvd CITY: South San Bruno Blvd CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                            PLING DATE: 1920306
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-May 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705212
FILING DATE: 25-Sep-1991
PRIOR APPLICATION NUMBER: 07/70801
FILING DATE: 08-No. 5367060-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hensley: Max D.
                                                                                                                                                                                                                                                                            US/07/847,743B
STREET: 460 Point San Bruno Blvd
CTTY: South Sar. Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                    PC-DOS/MS-DOS
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                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                    SOFTWARE: patin (Generated)
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/07/8
FILING DATE: 19920306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1489
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
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                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY. U.S.A.

ZIP: 20005-3918

ZIP: 20005-3918

COMPUTER READALE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,481
FILING DATE: 28-DEC-1993
CLASSIFICATION NUMBER: US 07/922,521
FILING DATE: 30-JUL-1992
ATFORNEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 16,733
REGISTRATION NUMBER: 16,733
REGISTRATION NUMBER: 16,733
                                                                                                                                                                                                                                                                                                                                                 Query Match 41.0%; Score 113.5; DB 1;
Best Local Similarity 34.8%; Pred. No. 2.9e-06;
Matches 16; Conservative 14; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP
TELECOMMUNICATION: TELEPHONE: / 2007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: CARCAMAY, KERMIT L.
APPLICANT: CARCAMAY, CORALIE A.
APPLICANT: FREGIEN, NEVIS L.
TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
NUMBER OF SEQUENCES: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-179-481-111
; Sequence 111, Application US/08179481
; Patent No. 5624816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 111:
                                       REFERENCE/DOCKET NUMBER: 71.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
NAME: Hensley, Max D. REGISTRATION NUMBER: 27,043
                                                                                                              TELEFAX: 415/952-9881
TELEX: 910/371-7168
INPORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 amino acids
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; MOLECULE TYPE: peptide
US-08-179-481-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                   linear
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Best Local Similarity
                                                                                                                                                                                                                                                              ; TOPOLOGY:
US-07-847-743B-26
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COUNTRY:
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Sequence 26, Application US/07847743B

Sequence 26, Application US/07847743B

Patent No. 5367060

GENERAL INFORMATION:

TITLE OF INVENTION: Structure, Production and Use of TITLE OF INVENTION: Herequlin

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 HLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 41.0%; Score 113.5; DB 1; Best Local Similarity 34.8%; Pred. No. 4.1e-07; Matches 16; Conservative 14; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRANT SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
FILLING DATE: 19920306
                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-May-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
FILING DATE: 25-Sep-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-NO. 5367060-1991
ATTORNEY AGENT INFORMATION:
                          APPLICATION NUMBER: US/07/847,743B FILING DATE: 19920306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/790801
FILING DATE: 08-No. 5367060-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-May-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/755212
FILING DATE: 25-Sep-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             NAME: Hensley, Max D.
REGISTRATION NUMBER: 27,043
REPRENCE/DOCKET NUMBER: 712P:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/256-1489
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: AMINO ACID
    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94080
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US-07-847-743B-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 HLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCOPGFTGARCTE 47
                                        Structure, Production and Use of Heregulin 2 Ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Production and Use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         b; Score 113.5; DB 1;
b; Pred. No. 2.8e-07;
14; Mismatches 15;
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Vandien, Richard L.,
APPLICANT: Holmes, William E.
TITLE OF INVENTION: Structure, Production TITLE OF INVENTION: Heregulin 2 Ligands NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                              TITLE OF INVENTION: Structure, Produc
TITLE OF INVENTION: Structure, Produc
TITLE OF INVENTION: Heregulin 2 Ligar
NUMBER OF SEQUENCES: 30
CORRESPONDENCE 30
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,145
                                                                                                                                                                                                                                                                                                                SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
APPLICATION NURBER: 07/880,917
PRIOR APPLICATION NURBER: 07/705256
PRIOR APPLICATION DATA:
APPLICATION NURBER: 07/765212
APPLICATION NURBER: 07/76512
APPLICATION NURBER: 07/765012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Genentech, Inc.
460 Point San Bruno Blvd
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Patent No. 5641869
GENERAL INFORMATIUM:
    Richard L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hensley, Max D.
REGISTRATION NUMBER: 27,034
REFERENCE/DOCKET NUMBER: 71.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1489
                      Holmes, William E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.0%;
34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            South San Francisco
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 415/266-1489
415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 34.89
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 amino acids
  Vandlen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                               COUNTRY: US ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-456-201-10
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US-08-456-201-13
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                        APPLICANT
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    Gaps
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  1;
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  15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                          1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                             APPLICANT: Vandlen, Richard L.,
APPLICANT: Vandlen, Milliam E.
TITLE OF INVENTION: Structure, Production and Use of
TITLE OF INVENTION: Heregulin 2 Ligands
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches
  14; Mismatches
                                                                                                                                                                                                                                                                                                          TABLEST: CONNTRY: USP

COUNTRY: USP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION NUMBER: 07/880,917
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08456201 Patent No. 5641869
                                                                                                                                                  US-08-456-201-8; Sequence 8, Application US/08456201; Patent No. 5641869; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 712 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
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415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 41.0%
Best Local Similarity 34.8%
Matches 16; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hensley, Max D. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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US-08-456-201-10
  16;
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  Matches
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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Structure, Production and Use of TITLE OF INVENTION: Heregulin 2 Ligands
UNMER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 113.5; DB 1;
Pred. No. 4.1e-07;
14; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Genentech, 1UC.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                PRIOR APPLICATION NOMBER: 07/765212
RAPPLICATION NUMBER: 07/765212
PAPLICATION NUMBER: 07/765212
APPLICATION NUMBER: 07/790801
ATTORNEY/AGENT INFORMATION:
NAME: Hensley, Max D.
REFERENCE/DOCKET NUMBER: 27,034
REFERENCE/DOCKET NUMBER: 712P4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415/266-1489
TELEFXX: 415/266-1489
TELEFXX: 415/266-1489
TELEFXX: 910/371-7168
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 aming acids
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APPLICATION NUMBER: 07/880,917
PRIOR APPLICATION NUMBER: 07/705256
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 26, Application US/08456201
; Patent No. 5641869
; GENERAL INFORMATION:
       07/880,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Vandlen, Richard L., APPLICANT: Holmes, William E.
                          PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/705256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 16; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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US-08-456-201-14
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US-08-456-201-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 HLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 41.0%; Score 113.5; DB 1
Best Local Similarity 34.8%; Pred. No. 3.1e-06;
Matches 16; Conservative 14; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08456201
Patent No. 5641869
GENERAL INFORMATION:
APPLICANT: Holmes, William E.
TITLE OF INVENTION: Structure, Production
TITLE OF INVENTION: Heregulin 2 Ligands
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
TREET: 460 Point San Bruno Blvd
CITY: SOUTH San Francisco
STRATE: California
COUNTRY: USA
                                                                                                                                                            FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,201
                                                                                                                                           APPLICATION NUMBER: US/08/456,201
                                                                                                                                                                                                                                                                          PILING APPLICATION NUMBER: 07/880,917
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
ATTONNEY/AGGNT INFORMATION:
NAME: Hensley, Max D.
REGISTRATION NUMBER: 27,034
                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 712P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/26-1489
TELEFAX: 415/35-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                             SOFTWARE: patin (Genentech)
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27,034

NAME: Hensley, Max D. REGISTRATION NUMBER:

FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,145
FILING DATE:

REFERENCE/DOCKET NUMBER: 71 TELECOMMUNICATION INFORMATION:

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Gaps
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                                                                                                                                                                                                                                                                                 Query Match
41.0%; Score 113.5; DB 1; Length 625;
Best Local Similarity 34.8%; Pred. No. 2.9e-06;
Matches 16; Conservative 14; Mismatches 15; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.0%; Score 113.5; DB 1; Length 52; 34.8%; Pred. No. 2.2e-07; tive 14; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,640A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08417640A
; Sequence 3, Application US/08417640A
; Patent No. 5670342
; GENERAL INFORMATION:
   APPLICANT: Carnahan, Josette F.
   APPLICANT: Hara, Shinichi
   APPLICANT: Hayer, John P.
   APPLICANT: Mayer, John P.
   CORRESPONDENCE ADDRESS:
   APPLICANT: Angen Inc.
   STATE: Angen Inc.
   STATE: Callifornia
   COMPTRY: GAL
   ABONESSE:
   ARBORDESE:
   COMPUTER READABLE FORM:
   ABONESSE:
   APPLICANT: MEDIUM TYPE: FLORDER.
: JULEPHANE: 415/266-1489

: TELEX: 415/952-981

: TELEX: 910/371-7168

: SEQUENCE CHARACIERISTICS:

LENGTH: 625 amin - TYPF.
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ATOMER'AGENT INFORMATION:
NAME: MAZZA, RICHARD J.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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; MOLECULE TYPE: protein
US-08-417-640A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 16; Conserva
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TOPOLOGY:
US-08-456-201-26
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Search completed: October 14, 1999, 00:43:10 Job time: 645 sec THIS PAGE BLANK (USPTO)